==========

Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=7; day=7; hr=13; min=15; sec=48; ms=415;]

==========

Validated By CRFValidator v 1.0.3

Application No: 10593846 Version No: 1.0

Input Set:

Output Set:

Started: 2008-06-30 20:05:23.923
Finished: 2008-06-30 20:05:24.292
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 369 ms
Total Warnings: 2
Total Errors: 0
No. of SeqIDs Defined: 12
Actual SeqID Count: 12

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)

SEQUENCE LISTING

<110> DIVERSA CORPORATION
BARTON, Nelson R.
O'DONOGHUE, Eileen
SHORT, Ryan
FREY, Gerhard
WEINER, David
ROBERTSON, Dan E.
BRIGGS, Steven
ZORNER, Paul

<120> CHIMERIC CANNULAE PROTEINS, NUCLEIC ACIDS ENCODING THEM AND METHODS FOR MAKING AND USING THEM

<130> 564462006801

<140> 10593846
<141> 2008-06-30

<150> PCT/US2005/009927
<151> 2005-03-24

<150> 60/556,393
<151> 2004-03-24

<150> 60/605,192
<151> 2004-08-27

<160> 12

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 624
<212> DNA
<213> Pyrodictium abyssi

<400> 1
gtgaagtaca caaccctagc tatagcgggt attattgcct cggctgccgc cctcgccctc 60
ctagcaggct tcgccaccac ccagagcccc ctcaacagct tctacgccac cggtacagca 120
caggcagtaa gcgagccaat agacgtagaa agccacctcg gcagcataac ccccgcagcc 180
ggcgcacagg gcagtgacga cataggttac gcaatagtgt ggataaagga ccaggtcaat 240
gatgtaaagc tgaaggtgac cctgcgtaac gctgagcagc taaagcccta cttcaagtac 300
ctacagatac agataacaag cggctatgag acgaacagca cagctctagg caacttcagc 360
gagaccaagg ctgtgataag cctcgacaac cccagcgccg tgatagtact agacaaggag 420
gatatagcag tgctctatcc ggacaagacc ggttacacaa acacttcgat atgggtaccc 480
ggtgaacctg acaagataat tgtctacaac gagacaaagc cagtagctat actgaacttc 540
aaggccttct acgaggctaa ggagggtatg ctattcgaca gcctgccagt gatattcaac 600
ttccaggtgc tacaagtagg ctaa 624

<210> 2
<211> 207
<212> PRT
<213> Pyrodictium abyssi

<400> 2

```
Val Lys Tyr Thr Thr Leu Ala Ile Ala Gly Ile Ile Ala Ser Ala Ala
 1               5                  10                  15
Ala Leu Ala Leu Leu Ala Gly Phe Ala Thr Thr Gln Ser Pro Leu Asn
            20                  25                  30
Ser Phe Tyr Ala Thr Gly Thr Ala Gln Ala Val Ser Glu Pro Ile Asp
        35                  40                  45
Val Glu Ser His Leu Gly Ser Ile Thr Pro Ala Ala Gly Ala Gln Gly
    50                  55                  60
Ser Asp Asp Ile Gly Tyr Ala Ile Val Trp Ile Lys Asp Gln Val Asn
65                  70                  75                  80
Asp Val Lys Leu Lys Val Thr Leu Arg Asn Ala Glu Gln Leu Lys Pro
                85                  90                  95
Tyr Phe Lys Tyr Leu Gln Ile Gln Ile Thr Ser Gly Tyr Glu Thr Asn
            100                 105                 110
Ser Thr Ala Leu Gly Asn Phe Ser Glu Thr Lys Ala Val Ile Ser Leu
        115                 120                 125
Asp Asn Pro Ser Ala Val Ile Val Leu Asp Lys Glu Asp Ile Ala Val
    130                 135                 140
Leu Tyr Pro Asp Lys Thr Gly Tyr Thr Asn Thr Ser Ile Trp Val Pro
145                 150                 155                 160
Gly Glu Pro Asp Lys Ile Ile Val Tyr Asn Glu Thr Lys Pro Val Ala
                165                 170                 175
Ile Leu Asn Phe Lys Ala Phe Tyr Glu Ala Lys Glu Gly Met Leu Phe
            180                 185                 190
Asp Ser Leu Pro Val Ile Phe Asn Phe Gln Val Leu Gln Val Gly
        195                 200                 205
```

<210> 3

<211> 513

<212> DNA

<213> Pyrodictium abyssi

<400> 3

```
gtgaagccta cggctctagc cctggctggt atcattgcct cggctgccga cctcgccctg      60
ctagcaggct tcgccaccac ccagagcccg ctcaacagct tctacgccac cggcacagca     120
gccgcaacaa gcgagccaat agacgtagag agccacctca gcagcatagc ccctgctgct     180
ggcgcacagg gcagccagga cataggctac ttcaacgtga ccgccaagga tcaagtgaac     240
gtgacaaaga taaaggtgac cctggctaac gctgagcagc taaagcccta cttcaagtac     300
ctacagatag tgctaaagag cgaggtagct gacgagatca aggccgtaat aagcatagac     360
aagcctagcg ccgtcataat actagacagc caggacttcg acagcaacaa cagagcaaag     420
ataagcgcca ctgcctacta cgaggctaag gagggcatgc tattcgacag cctaccgcta     480
atattcaaca tacaggtgct aagcgtcagc taa                                  513
```

<210> 4

<211> 170

<212> PRT

<213> Pyrodictium abyssi

<400> 4

```
Val Lys Pro Thr Ala Leu Ala Leu Ala Gly Ile Ile Ala Ser Ala Ala
 1               5                  10                  15
Asp Leu Ala Leu Leu Ala Gly Phe Ala Thr Thr Gln Ser Pro Leu Asn
            20                  25                  30
Ser Phe Tyr Ala Thr Gly Thr Ala Ala Ala Thr Ser Glu Pro Ile Asp
        35                  40                  45
Val Glu Ser His Leu Ser Ser Ile Ala Pro Ala Ala Gly Ala Gln Gly
```

```
    50                  55                  60
Ser Gln Asp Ile Gly Tyr Phe Asn Val Thr Ala Lys Asp Gln Val Asn
65                  70                  75                  80
Val Thr Lys Ile Lys Val Thr Leu Ala Asn Ala Glu Gln Leu Lys Pro
                85                  90                  95
Tyr Phe Lys Tyr Leu Gln Ile Val Leu Lys Ser Glu Val Ala Asp Glu
            100                 105                 110
Ile Lys Ala Val Ile Ser Ile Asp Lys Pro Ser Ala Val Ile Ile Leu
        115                 120                 125
Asp Ser Gln Asp Phe Asp Ser Asn Asn Arg Ala Lys Ile Ser Ala Thr
    130                 135                 140
Ala Tyr Tyr Glu Ala Lys Glu Gly Met Leu Phe Asp Ser Leu Pro Leu
145                 150                 155                 160
Ile Phe Asn Ile Gln Val Leu Ser Val Ser
                165                 170
```

<210> 5
<211> 537
<212> DNA
<213> Pyrodictium abyssi

<400> 5
atgaggtaca cgaccctagc tctggccggc atagtggcct cggctgccgc cctcgccctg 60
ctagcaggct tcgccacgac ccagagcccg ctaagcagct tctacgccac cggcacagca 120
caagcagtaa gcgagccaat agacgtagag agccacctag acaacaccat agcccctgct 180
gccggtgcac agggctacaa ggacatgggc tacattaaga taactaacca gtcaaaagtt 240
aatgtaataa agctgaaggt gactctcgct aacgccgagc agctaaagcc ctacttcgac 300
tacctacagc tagtactcac aagcaacgcc actggcaccg acatggttaa ggctgtgcta 360
agcctcgaga agcctagcgc agtcataata ctagacaacg atgactacga tagcactaac 420
aagatacagc taaaggtaga agcctactat gaggctaagg agggcatgct attcgacagc 480
ctaccagtaa tactgaactt ccaggtactg agcgccgctt gcagtccctt gtggtga 537

<210> 6
<211> 178
<212> PRT
<213> Pyrodictium abyssi

<400> 6
```
Met Arg Tyr Thr Thr Leu Ala Leu Ala Gly Ile Val Ala Ser Ala Ala
 1               5                  10                  15
Ala Leu Ala Leu Leu Ala Gly Phe Ala Thr Thr Gln Ser Pro Leu Ser
            20                  25                  30
Ser Phe Tyr Ala Thr Gly Thr Ala Gln Ala Val Ser Glu Pro Ile Asp
        35                  40                  45
Val Glu Ser His Leu Asp Asn Thr Ile Ala Pro Ala Ala Gly Ala Gln
    50                  55                  60
Gly Tyr Lys Asp Met Gly Tyr Ile Lys Ile Thr Asn Gln Ser Lys Val
65                  70                  75                  80
Asn Val Ile Lys Leu Lys Val Thr Leu Ala Asn Ala Glu Gln Leu Lys
                85                  90                  95
Pro Tyr Phe Asp Tyr Leu Gln Leu Val Leu Thr Ser Asn Ala Thr Gly
            100                 105                 110
Thr Asp Met Val Lys Ala Val Leu Ser Leu Glu Lys Pro Ser Ala Val
        115                 120                 125
Ile Ile Leu Asp Asn Asp Asp Tyr Asp Ser Thr Asn Lys Ile Gln Leu
    130                 135                 140
Lys Val Glu Ala Tyr Tyr Glu Ala Lys Glu Gly Met Leu Phe Asp Ser
```

145 150 155 160
Leu Pro Val Ile Leu Asn Phe Gln Val Leu Ser Ala Ala Cys Ser Pro
165 170 175
Leu Trp

<210> 7
<211> 395
<212> DNA
<213> Pyrodictium abyssi

<400> 7
agcttctacg ccaccggcac agcacaggca gtaagcgagc caatagacgt ggtaagcagc 60
ctcggtacgc taaatactgc cgctggtgca cagggtaagc agacgctagg agacataaca 120
atatatgcgc acaatgacgt gaacataaca aagctaaagg tcacgcttgc taacgctgca 180
cagctaagac catacttcaa gtacctgata ataaagctag taagcctgga cagcaacggc 240
aacgagtccg aggaaaaggg catgataact ctatggaagc cttacgccgt gataatacta 300
gaccatgaag atttcaacaa cgacatcgac aatgacggca acaatgacgc caagataagg 360
gttgtagcct actatgaggc taaggagggt atgct 395

<210> 8
<211> 131
<212> PRT
<213> Pyrodictium abyssi

<400> 8
Ser Phe Tyr Ala Thr Gly Thr Ala Gln Ala Val Ser Glu Pro Ile Asp
1 5 10 15
Val Val Ser Ser Leu Gly Thr Leu Asn Thr Ala Ala Gly Ala Gln Gly
20 25 30
Lys Gln Thr Leu Gly Asp Ile Thr Ile Tyr Ala His Asn Asp Val Asn
35 40 45
Ile Thr Lys Leu Lys Val Thr Leu Ala Asn Ala Ala Gln Leu Arg Pro
50 55 60
Tyr Phe Lys Tyr Leu Ile Ile Lys Leu Val Ser Leu Asp Ser Asn Gly
65 70 75 80
Asn Glu Ser Glu Glu Lys Gly Met Ile Thr Leu Trp Lys Pro Tyr Ala
85 90 95
Val Ile Ile Leu Asp His Glu Asp Phe Asn Asn Asp Ile Asp Asn Asp
100 105 110
Gly Asn Asn Asp Ala Lys Ile Arg Val Val Ala Tyr Tyr Glu Ala Lys
115 120 125
Glu Gly Met
130

<210> 9
<211> 372
<212> DNA
<213> Pyrodictium abyssi

<400> 9
agcttctacg ccaccggcac agcagaggca acaagcgagc caatagacgt tgtaagcaac 60
cttaacacgg ccatagcccc tgctgccggc gcccagggca gcgtgggcat aggcagcata 120
acaatagaga acaagactga cgtgaacgtt gtgaagctga agataaccct cgccaacgct 180
gagcagctaa agccctactt cgactaccta cagatagtgc taaagagcgt tgacagcaac 240
gagatcaagg ctgtgctaag cctcgagaag cccagcgcag tcataatact ggacaacgag 300
gacttccagg gcggcgacaa ccagtgccag atagacgcca ccgcctacta cgaggctaag 360
gagggtatgc ta 372

<210> 10
<211> 124
<212> PRT
<213> Pyrodictium abyssi

<400> 10
Ser Phe Tyr Ala Thr Gly Thr Ala Glu Ala Thr Ser Glu Pro Ile Asp
 1   5   10   15
Val Val Ser Asn Leu Asn Thr Ala Ile Ala Pro Ala Ala Gly Ala Gln
            20   25   30
Gly Ser Val Gly Ile Gly Ser Ile Thr Ile Glu Asn Lys Thr Asp Val
        35   40   45
Asn Val Val Lys Leu Lys Ile Thr Leu Ala Asn Ala Glu Gln Leu Lys
    50   55   60
Pro Tyr Phe Asp Tyr Leu Gln Ile Val Leu Lys Ser Val Asp Ser Asn
65   70   75   80
Glu Ile Lys Ala Val Leu Ser Leu Glu Lys Pro Ser Ala Val Ile Ile
                85   90   95
Leu Asp Asn Glu Asp Phe Gln Gly Gly Asp Asn Gln Cys Gln Ile Asp
            100   105   110
Ala Thr Ala Tyr Tyr Glu Ala Lys Glu Gly Met Leu
        115   120

<210> 11
<211> 448
<212> DNA
<213> Artificial Sequence

<220>
<223> consensus sequence

<400> 11
tgagacccta gctgcggatt gcctcggctg ccgcctcgcc ctctagcagg cttcgccaca 60
cccagagccc ctacagcttc tacgccaccg gcacagcaca ggcagtaagc gagccaatag 120
acgtagaaag ccacctcaca catagcccct gctgccggcg cacagggcag caggacatag 180
gctacataaa ataacaagat agtgaacgta taaagctgaa ggtgaccctg ctaacgctga 240
gcagctaaag ccctacttca agtacctaca gatagtgcta aaagcgacag caggcacacg 300
agaaggcgtg ataagcctcg agaagcctag cgccgtcata atactagaca acgaggactt 360
cgaagcacaa cagaaagaga agcaatagcc tactacgagg ctaaggaggg tatgctattc 420
gacagcctcc tatataactc aggtctgt   448

<210> 12
<211> 140
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<400> 12
Val Lys Thr Leu Ala Leu Ala Gly Ile Ile Ala Ser Ala Ala Leu Ala
 1   5   10   15
Leu Leu Ala Gly Phe Ala Thr Thr Gln Ser Pro Leu Ser Phe Tyr Ala
            20   25   30
Thr Gly Thr Ala Gln Ala Val Ser Glu Pro Ile Asp Val Glu Ser His
        35   40   45

```
Leu Ser Ile Ala Pro Ala Ala Gly Ala Gln Gly Ser Asp Ile Gly Tyr
    50                  55                  60
Ile Ile Lys Val Asn Val Val Lys Leu Lys Val Thr Leu Ala Asn Ala
65                  70                  75                  80
Glu Gln Leu Lys Pro Tyr Phe Lys Tyr Leu Gln Ile Val Leu Ser Ser
                85                  90                  95
Glu Ile Lys Ala Val Ile Ser Leu Asp Lys Pro Ser Ala Val Ile Ile
            100                 105                 110
Leu Asp Glu Asp Phe Ala Ile Ala Tyr Tyr Glu Ala Lys Glu Gly Met
        115                 120                 125
Leu Phe Asp Ser Leu Pro Val Ile Asn Gln Val Leu
    130                 135                 140
```